



## SEQUENCE LISTING

Hoogenboom, Hendricus R.J.M.  
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<120> MUCIN-1 SPECIFIC BINDING MEMBERS AND  
METHODS OF USE THEREOF

<130> 10280-075002

<140> US 09/822,698

<141> 2001-03-30

<150> US 09/538,913

<151> 2000-03-30

<160> 116

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 113

<212> PRT

<213> Artificial Sequence

<220>

<223> light chain variable region of the MUC1- specific  
binding domain of PH1 Fab antibody

<400> 1

Glu	Ile	Val	Leu	Thr	Gln	Ser	Pro	Leu	Ser	Leu	Pro	Val	Thr	Pro	Gly
1				5					10					15	
Glu	Pro	Ala	Ser	Ile	Ser	Cys	Arg	Ser	Ser	Gln	Ser	Leu	Leu	His	Ser
			20					25				30			
Asn	Gly	Tyr	Thr	Tyr	Leu	Asp	Trp	Tyr	Leu	Gln	Lys	Pro	Gly	Gln	Ser
		35				40					45				
Pro	Gln	Leu	Leu	Ile	Tyr	Ser	Gly	Ser	His	Arg	Ala	Ser	Gly	Val	Pro
	50				55				60						
Asp	Arg	Phe	Ser	Gly	Ser	Val	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Arg	Ile
65				70				75					80		
Ser	Arg	Val	Glu	Ala	Glu	Asp	Val	Gly	Val	Tyr	Tyr	Cys	Met	Gln	Gly
			85					90					95		
Leu	Gln	Ser	Pro	Phe	Thr	Phe	Gly	Pro	Gly	Thr	Lys	Val	Asp	Ile	Lys
			100					105					110		
Arg															

<210> 2

<211> 339

<212> DNA

<213> Artificial Sequence

<220>

<223> nucleotide sequence coding of light chain variable  
region of the MUC1- specific binding domain of PH1  
Fab antibody

<400> 2  
 gaaattgtgc tgactcagtc tccactctcc ctgcccgctca cccctggaga gccggcctcc 60  
 atctcctgca ggtctagtca gagcctcctg catagtaatg gatacaccta tttggattgg 120  
 tacctgcaga agccagggca gtctccacag ctctctgatct attcgggttc tcatcggggc 180  
 tccgggggtcc ctgacagggt cagtggcagt gtatcaggca cagattttac actgagaatc 240  
 agcagagtgg aggctgagga tggtggagtt tattactgca tgcagggtct acagagtcca 300  
 ttcactttcg gccctgggac caaagtggat atcaaacga 339

<210> 3  
 <211> 121  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> heavy chain variable region of the MUC1- specific  
 binding domain of PH1 Fab antibody

<400> 3  
 Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
 1 5 10 15  
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Ser Asn  
 20 25 30  
 Ala Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45  
 Ser Gly Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val  
 50 55 60  
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
 65 70 75 80  
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95  
 Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Asp Tyr Trp Gly  
 100 105 110  
 Gln Gly Thr Leu Val Thr Val Ser Ser  
 115 120

<210> 4  
 <211> 363  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> nucleotide sequence coding of heavy chain variable  
 region of the MUC1- specific binding domain of PH1  
 Fab antibody

<400> 4  
 cagggtccagc tgggtgcagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60  
 tcctgtgcag cctctggatt caggtttaga agtaacgcc a tgggctgggt ccgccaggct 120  
 ccagggaagg ggctggagtg ggtctcagggt attagtggta gtggtggcag cacatactac 180  
 gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cagctgttat 240  
 ctgcaaataga acagcctgag agcogaggac acggccgtat attattgtgc gaaacatacc 300  
 gggggggggcg tttgggaccc cattgactac tggggccagg gaaccctggt caccgtctca 360  
 agc 363

<210> 5  
 <211> 381

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; MUC1-specific immunocytokine bivPH1-IL-2

&lt;400&gt; 5

Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
 1 5 10 15  
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Ser Asn  
 20 25 30  
 Ala Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45  
 Ser Gly Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val  
 50 55 60  
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
 65 70 75 80  
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95  
 Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Asp Tyr Trp Gly  
 100 105 110  
 Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ala Leu Glu Ile  
 115 120 125  
 Val Leu Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly Glu Pro  
 130 135 140  
 Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser Asn Gly  
 145 150 155 160  
 Tyr Thr Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Gln  
 165 170 175  
 Leu Leu Ile Tyr Ser Gly Ser His Arg Ala Ser Gly Val Pro Asp Arg  
 180 185 190  
 Phe Ser Gly Ser Val Ser Gly Thr Asp Phe Thr Leu Arg Ile Ser Arg  
 195 200 205  
 Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Gly Leu Gln  
 210 215 220  
 Ser Pro Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg Gly  
 225 230 235 240  
 Gly Gly Ser Gly Gly Gly Ala Leu Ala Pro Thr Ser Ser Ser Thr Lys  
 245 250 255  
 Lys Thr Gln Leu Gln Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile  
 260 265 270  
 Leu Asn Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu  
 275 280 285  
 Thr Phe Lys Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu  
 290 295 300  
 Gln Cys Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu Val Leu Asn Leu  
 305 310 315 320  
 Ala Gln Ser Lys Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn  
 325 330 335  
 Ile Asn Val Ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met  
 340 345 350  
 Cys Glu Tyr Ala Asp Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg  
 355 360 365  
 Trp Ile Thr Phe Cys Gln Ser Ile Ile Ser Thr Leu Thr  
 370 375 380

&lt;210&gt; 6

<211> 1143  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> MUC1-specific immunocytokine bivPH1-IL-2

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 caggtccagc tgggtgcagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60  
 tcctgtgcag cctctggatt cacgtttaga agtaacgcc a tgggctgggt ccgccaggct 120  
 ccagggaagg ggctggagtg ggtctcaggt attagtggta gtgggtggcag cacatactac 180  
 gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240  
 ctgcaaatga acagcctgag agccgaggac acggccgtat attattgtgc gaaacatacc 300  
 gggggggggcg tttgggaccc cattgactac tggggccagg gaaccctggg caccgtctca 360  
 agcggaggcg gtgcacttga aattgtgctg actcagtctc cactctccct gcccgtcacc 420  
 cctggagagc cggcctccat ctctgcagg tctagtcaga gcctcctgca tagtaatgga 480  
 tacacctatt tggattggta cctgcagaag ccagggcagt ctccacagct cctgatctat 540  
 tcgggttctc atcgggcctc cggggtccct gacaggttca gtggcagtg atcaggcaca 600  
 gattttacac tgagaatcag cagagtggag gctgaggatg ttggagttta ttactgcatg 660  
 cagggtctac agagtccatt cactttcggc cctgggacca aagtggatat caaacgaggg 720  
 ggtggatcag gcggcggggc cctagcacct acttcaagtt ctacaaagaa aacacagcta 780  
 caactggagc atttactgct ggattttacag atgattttga atggaattaa taattacaag 840  
 aatcccaaac tcaccaggat gtcacattt aagttttaca tgcccaagaa ggccacagaa 900  
 ctgaaacatc ttcagtgtct agaagaagaa ctcaaacctc tggaggaagt gctaaattta 960  
 gctcaaagca aaaactttca cttaagacct agggacttaa tcagcaatat caacgtaata 1020  
 gttctggaac taaagggatc tgaaacaaca ttcattgtgtg aatatgctga tgagacagca 1080  
 accattgtag aatttctgaa cagatggatt accttttgtc aaagcatcat ctcaacactg 1140  
 act 1143

<210> 7  
 <211> 20  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> peptide of MUC1 protein

<400> 7  
 Pro Ala His Gly Val Thr Ser Ala Pro Asp Thr Arg Pro Ala Pro Gly  
 1 5 10 15  
 Ser Thr Ala Pro  
 20

<210> 8  
 <211> 20  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> peptide of MUC1 protein

<400> 8  
 Val Thr Ser Ala Pro Asp Thr Arg Pro Ala Pro Gly Ser Thr Ala Pro  
 1 5 10 15  
 Pro Ala His Gly  
 20

<210> 9  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> CH1FOR primer  
  
 <400> 9  
 gtccttgacc aggcagccca gggc 24  
  
 <210> 10  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> pUC-reverse primer  
  
 <400> 10  
 agcggataac aatttcacac agg 23  
  
 <210> 11  
 <211> 44  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> VL backward primer  
  
 <400> 11  
 accgcctcca ccagtgcact tgaaattgtg ctgactcagt ctcc 44  
  
 <210> 12  
 <211> 51  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> VL forward primer  
  
 <400> 12  
 accgcctcca ccgggcgcgc cttattaaca ctctcccctg ttgaagctct t 51  
  
 <210> 13  
 <211> 61  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> VL backward primer for light chain variable region  
 of the PH1 Fab antibody with additional linker and  
 restriction sites  
  
 <400> 13  
 gccgatcgct ctggtcaccg tctcaagcgg aggcgggtgca cttgaaattg tgctgactca 60  
 g 61

<210> 14  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> VL forward primer for light chain variable region  
 of the PH1 Fab antibody with additional linker and  
 restriction sites  
  
 <400> 14  
 gtctcgcgag cggccgcccga ttggatatcc actttggtcc cagggccgaa 50  
  
 <210> 15  
 <211> 27  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> nucleotide sequence coding for a nine amino acid  
 linker  
  
 <400> 15  
 ggggggtggat cagggcggcgg ggccta 27  
  
 <210> 16  
 <211> 69  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> PH1-IL-2 backward primer  
  
 <400> 16  
 accaaagtgg atatcaaacg aggggggtgga tcaggcggcg gggccctagc acctacttca 60  
 agttctaca 69  
  
 <210> 17  
 <211> 49  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> PH1-IL-2 forward primer  
  
 <400> 17  
 gtcccgcgtg cggccgcagt cagtgttgag atgatgcttt gacaaaagg 49  
  
 <210> 18  
 <211> 98  
 <212> PRT  
 <213> Artificial Sequence  
  
 <220>  
 <223> heavy chain variable region from a DP47 germ line

&lt;400&gt; 18

Glu	Val	Gln	Leu	Leu	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly
1				5					10					15	
Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Ser	Ser	Tyr
			20					25					30		
Ala	Met	Ser	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val
	35						40					45			
Ser	Ala	Ile	Ser	Gly	Ser	Gly	Gly	Ser	Thr	Tyr	Tyr	Ala	Asp	Ser	Val
	50					55					60				
Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Thr	Leu	Tyr
65					70					75				80	
Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
			85						90					95	

Ala Lys

&lt;210&gt; 19

&lt;211&gt; 100

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; light chain variable region from a DP47 germ line

&lt;400&gt; 19

Asp	Ile	Val	Met	Thr	Gln	Ser	Pro	Leu	Ser	Leu	Pro	Val	Thr	Pro	Gly
1				5					10					15	
Glu	Pro	Ala	Ser	Ile	Ser	Cys	Arg	Ser	Ser	Gln	Ser	Leu	Leu	His	Ser
			20					25				30			
Asn	Gly	Tyr	Asn	Tyr	Leu	Asp	Trp	Tyr	Leu	Gln	Lys	Pro	Gly	Gln	Ser
	35					40					45				
Pro	Gln	Leu	Leu	Ile	Tyr	Leu	Gly	Ser	Asn	Arg	Ala	Ser	Gly	Val	Pro
	50				55					60					
Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Lys	Ile
65					70				75					80	
Ser	Arg	Val	Glu	Ala	Glu	Asp	Val	Gly	Val	Tyr	Tyr	Cys	Met	Gln	Ala
			85						90					95	

Leu Gln Thr Pro  
100

&lt;210&gt; 20

&lt;211&gt; 14

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; myc tag peptide

&lt;400&gt; 20

Glu	Gln	Lys	Leu	Ile	Ser	Glu	Glu	Asp	Leu	Asn	Gly	Ala	Ala
1				5						10			

&lt;210&gt; 21

&lt;211&gt; 42

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

<220>

<223> nucleotide sequence coding of myc tag peptide

<400> 21

gaacaaaaac tcatctcaga agaggatctg aatggggccg ca

42

<210> 22

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> hexahistidine peptide

<400> 22

His His His His His His

1

5

<210> 23

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> nucleotide sequence coding of hexahistidine peptide

<400> 23

catcaccatc atcaccat

18

<210> 24

<211> 220

<212> PRT

<213> Artificial Sequence

<220>

<223> immunoglobulin kappa light chain of MUC1-specific PH1-IgG1

<400> 24

Glu Ile Val Leu Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly  
1 5 10 15

Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser  
20 25 30

Asn Gly Tyr Thr Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser  
35 40 45

Pro Gln Leu Leu Ile Tyr Ser Gly Ser His Arg Ala Ser Gly Val Pro  
50 55 60

Asp Arg Phe Ser Gly Ser Val Ser Gly Thr Asp Phe Thr Leu Arg Ile  
65 70 75 80

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Gly  
85 90 95

Leu Gln Ser Pro Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys  
100 105 110

Arg Gly Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Ser Asp  
115 120 125

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn



130		135		140
Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu				
145		150		155
Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp				
	165		170	175
Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr				
	180		185	190
Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser				
	195		200	205
Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys				
210		215		220

<210> 25  
 <211> 663  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> nucleotide sequence coding of immunoglobulin kappa  
 light chain of MUC1-specific PH1-IgG1

<400> 25	
gaaattgtgc tgactcagtc tccactctcc ctgcccgtca cccctggaga gccggcctcc	60
atctcctgca ggtctagtca gagcctcctg catagtaatg gatacaccta tttggattgg	120
tacctgcaga agccagggca gtctccacag ctccctgatct attcgggttc tcatcggggcc	180
tccgggggtcc ctgacagggt cagtggcagt gtatcaggca cagattttac actgagaatc	240
agcagagtgg aggctgagga tgttgaggtt tattactgca tgcagggtct acagagtcca	300
ttcactttcg gccctgggac caaagtggat atcaaacgag gaactgtggc tgcaccatct	360
gtcttcatct tcccgccatc tgatgagcag ttgaaatctg gaactgcctc tgttgtgtgc	420
ctgctgaata acttctatcc cagagaggcc aaagtacagt ggaagggtga taacgcctc	480
caatcgggta actcccagga gagtgtcaca ggcaggaca gcaaggacag cacctacagc	540
ctcagcagca cccctgacgct gagcaaagca gactacgaga aacacaaagt ctacgcctgc	600
gaagtcaccc atcagggcct gagttcaccc gtgacaaaga gcttcaacag gggagagtgt	660
tag	663

<210> 26  
 <211> 451  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> immunoglobulin heavy chain of MUC1-specific  
 PH1-IgG1

<400> 26	
Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro Gly Gly	
1	15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Ser Asn	
20	30
Ala Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val	
35	45
Ser Gly Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val	
50	60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr	
65	80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys	
85	95

Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Asp Tyr Trp Gly  
 100 105 110  
 Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser  
 115 120 125  
 Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala  
 130 135 140  
 Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val  
 145 150 155 160  
 Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala  
 165 170 175  
 Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val  
 180 185 190  
 Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His  
 195 200 205  
 Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys  
 210 215 220  
 Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly  
 225 230 235 240  
 Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met  
 245 250 255  
 Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His  
 260 265 270  
 Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val  
 275 280 285  
 His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr  
 290 295 300  
 Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly  
 305 310 315 320  
 Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile  
 325 330 335  
 Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val  
 340 345 350  
 Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser  
 355 360 365  
 Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu  
 370 375 380  
 Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro  
 385 390 395 400  
 Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val  
 405 410 415  
 Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met  
 420 425 430  
 His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser  
 435 440 445  
 Pro Gly Lys  
 450

<210> 27

<211> 1356

<212> DNA

<213> Artificial Sequence

<220>

<223> nucleotide sequence coding of immunoglobulin heavy  
chain of MUC1-specific PH1-IgG1

<400> 27

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cagggtccagc tgggtgcagtc tgggggagggc ttggtacagc ctgggggggtc cctgagactc      60
tcctgtgcag cctctggatt cacgtttaga agtaacgcca tgggctgggt ccgccaggct      120
ccagggaagg ggctggagtg ggtctcaggt attagtggta gtgggtggcag cacatactac      180
gcagactccg tgaaggggccg gttcaccatc tccagagaca attccaagaa cacgctgtat      240
ctgcaaataga acagcctgag agccgaggac acggcgcgtat attattgtgc gaaacatacc      300
ggggggggcg tttgggaccc cattgactac tggggccagg gaaccctggt caccgtctca      360
agcgccctcca ccaaggggccc atcgggtcttc cccctggcac cctcctccaa gagcacctct      420
gggggacacag cggccctggg ctgcctggtc aaggactact tccccgaacc ggtgacggtg      480
tcgtggaact caggcgccct gaccagcggc gtccacacct tcccggtgt cctacagtcc      540
tcaggactct actccctcag cagcgtagt accgtgccct ccagcagctt gggcacccag      600
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ggacgcgtcag tcttctcttt cccccaaaaa cccaaggaca ccctcatgat ctcccgacc      780
cctgaggtca catgcgtggg ggtggacgtg agccacgaag accctgaggt caagttcaac      840
tggtagctgg acggcgtgga ggtgcataat gccaaagacaa agccgcggga ggagcagtac      900
aacagcacgt accgtgtggg cagcgtcctc accgtcctgc accaggactg gctgaatggc      960
aaggagtaca agtgcaaggc ctccaacaaa gccctcccag ccccatcga gaaaaccatc     1020
tccaaagcca aagggcagcc ccgagaacca cagggtgtaca ccctgcccc atcccgggat     1080
gagctgacca agaaccaggt cagcctgacc tgcttgggtc aaggcttcta tcccagcgac     1140
atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cagcctccc     1200
gtgctggact ccgacggctc cttcttctc tacagcaagc tcaccgtgga caagagcagg     1260
tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac     1320
acgcagaaga gcctctcctt aagtccggga aaataa                                1356

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<210> 28

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> MUC1-specific binding member

<221> VARIANT

<222> 1

<223> Xaa = Ala, Ser, Thr, or Val

<221> VARIANT

<222> 2

<223> Xaa = Lys, Ile Arg, or Gln

<221> VARIANT

<222> 3

<223> Xaa = Gly, Arg, Val, Glu, Ser, or Ala

<221> CONFLICT

<222> 4

<223> Xaa = Asp or Asn

<221> VARIANT

<222> 5

<223> Xaa = Ile, Leu, Met, Phe, or Val

<221> VARIANT

<222> (6)...(0)

<223> Xaa = Asp, Gly, Lys, Asn, Ala, His, Arg, Ser, Val,  
or Tyr

<221> VARIANT  
 <222> (7)...(0)  
 <223> Xaa = Tyr, His, Lys, Asn, Asp, Ser, or Pro  
  
 <400> 28  
 Xaa Xaa His Thr Gly Xaa Gly Val Trp Xaa Pro Xaa Xaa Xaa  
 1 5 10  
  
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 Ala Lys His Thr Gly Arg Gly Val Trp Asp Pro Ile Gly Tyr  
 1 5 10  
  
 <210> 30  
 <211> 14  
 <212> PRT  
 <213> Artificial Sequence  
  
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 <223> region of a MUC1-specific binding member  
  
 <400> 30  
 Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Lys His  
 1 5 10  
  
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 <211> 14  
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 <400> 31  
 Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Gly Tyr  
 1 5 10  
  
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 <400> 32  
 Ala Ile His Thr Gly Gly Gly Val Trp Asp Pro Ile Lys Tyr  
 1 5 10  
  
 <210> 33

<211> 33  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> primer

<221> misc\_feature  
 <222> 16, 17, 18  
 <223> n may be varied according to the disclosure to  
 form mutagenic primer

<400> 33  
 ggattcacgt ttagannnaa cgccatgggc tgg

33

<210> 34  
 <211> 39  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> primer

<221> misc\_feature  
 <222> 16, 17, 18 22, 23, 24  
 <223> n may be varied according to the disclosure to  
 form mutagenic primer sequences

<400> 34  
 cacggagtct gcgtannntg tnnngccacc actaccact

39

<210> 35  
 <211> 90  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> primer

<221> misc\_feature  
 <222> 34-75  
 <223> n may be varied according to the disclosure to  
 form mutagenic primer sequences

<400> 35  
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 nnnnnnnnnn nnnnnacaat aatatacggc

60

90

<210> 36  
 <211> 90  
 <212> DNA  
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<220>  
 <223> primer

<221> misc\_feature

<222> 56, 57, 59, 60, 62, 63, 65, 66, 68, 69

<223> n may be varied according to the disclosure to  
form mutagenic primer sequences

<400> 36

ctatgagacg gtgaccaggg ttccctggcc ccagtagtca atgggggtccc aaacmnnmnn 60  
mnnmnnmnnnt ttgcacaat aatatacggc 90

<210> 37

<211> 90

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<221> misc feature

<222> 41, 42, 44, 45, 47, 48, 50, 51, 53, 54

<223> n may be varied according to the disclosure to  
form mutagenic primer sequences

<400> 37

ctatgagacg gtgaccaggg ttccctggcc ccagtagtcm nnnnnnnnnn nmngccccc 60  
cccgtatgt ttgcacaat aatatacggc 90

<210> 38

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> HuJH4-5-FOR primer

<400> 38

tgaggagacg gtgaccaggg ttcc 24

<210> 39

<211> 56

<212> DNA

<213> Artificial Sequence

<220>

<223> VH1c back Sfi primer

<400> 39

gtcctcgcaa ctgcggccca gccggccatg gccsaggtcc agctggtrca gtctgg 56

<210> 40

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> PAP peptide epitope of MUC1 bound by PH1 Fab  
antibody

<400> 40

Pro Asp Thr Arg Pro Ala Pro Gly Ser Thr Ala Pro Pro Ala Leu  
 1 5 10 15

<210> 41  
 <211> 16  
 <212> PRT  
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<220>  
 <223> mutant CDR3 region of an antibody heavy chain  
 variable region

<400> 41  
 Ala Lys His Asn Thr Ser Lys Val Trp Asp Pro Ile Asp Tyr Trp Gly  
 1 5 10 15

<210> 42  
 <211> 48  
 <212> DNA  
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<220>  
 <223> nucleotide sequence coding for a mutant CDR3  
 region

<400> 42  
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48

<210> 43  
 <211> 16  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> mutant CDR3 region of an antibody heavy chain  
 variable region

<400> 43  
 Ala Lys Ser Ser Thr Thr Val Trp Asp Pro Ile Asp Tyr Trp Gly  
 1 5 10 15

<210> 44  
 <211> 48  
 <212> DNA  
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<220>  
 <223> nucleotide sequence coding for a mutant CDR3  
 region

<400> 44  
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48

<210> 45  
 <211> 16  
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<220>

<223> a mutant CDR3 region

<221> VARIANT

<222> 3

<223> Xaa indicates end of amino acid sequence because  
mutation in nucleotide sequence forms a  
translational stop codon

<400> 45

Ala	Lys	Xaa	Pro	Met	Ala	Asn	Val	Trp	Asp	Pro	Ile	Asp	Tyr	Trp	Gly
1				5				10						15	

<210> 46

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> nucleotide sequence coding for a mutant CDR3  
region

<400> 46

gcgaaatagc ctatggcgaa tgtttgggac cccattgact actggggc

48

<210> 47

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> mutant CDR3 region

<221> VARIANT

<222> 3

<223> Xaa indicates end of amino acid sequence because  
mutation in nucleotide sequence forms a  
translational stop codon

<400> 47

Ala	Lys	Xaa	His	Thr	Lys	Thr	Val	Trp	Asp	Pro	Ile	Asp	Tyr	Trp	Gly
1				5				10						15	

<210> 48

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> nucleotide sequence coding for a mutant CDR3  
region

<400> 48

gcgaaatagc atacgaagac ggtttgggac cccattgact actggggc

48

<210> 49



<211> 16  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> mutant CDR3 region of an antibody heavy chain  
 variable region

<400> 49  
 Ala Lys Ile Thr Val Ser Arg Val Trp Asp Pro Ile Asp Tyr Trp Gly  
 1 5 10 15

<210> 50  
 <211> 48  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> nucleotide sequence coding for a mutant CDR3  
 region

<400> 50  
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<210> 51  
 <211> 16  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> mutant CDR3 region of an antibody heavy chain  
 variable region

<400> 51  
 Ala Lys Arg Tyr Leu Tyr Asp Val Trp Asp Pro Ile Asp Tyr Trp Gly  
 1 5 10 15

<210> 52  
 <211> 48  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> nucleotide sequence coding for a mutant CDR3  
 region

<400> 52  
 gcgaaacgtt atctgtatga tgtttgggac cccattgact actggggc 48

<210> 53  
 <211> 16  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> mutant CDR3 region of an antibody heavy chain  
 variable region

<400> 53

Ala Lys His Thr Gly Gly Gly Thr Leu Gln Arg Leu Asp Tyr Trp Gly  
1 5 10 15

<210> 54

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> nucleotide sequence coding for a mutant CDR3  
region

<400> 54

gcgaaacata ccggggggggg cactttgcag cggctggact actggggc

48

<210> 55

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> mutant CDR3 region of an antibody heavy chain  
variable region

<400> 55

Ala Lys His Thr Gly Gly Gly Thr Gln Thr Pro Cys Asp Tyr Trp Gly  
1 5 10 15

<210> 56

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> nucleotide sequence coding for a mutant CDR3  
region

<400> 56

gcgaaacata ccggggggggg cactcagact ccgtgtgact actggggc

48

<210> 57

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> mutant CDR3 region of an antibody heavy chain  
variable region

<400> 57

Ala Lys His Thr Gly Gly Gly Arg Arg Ile Cys His Asp Tyr Trp Gly  
1 5 10 15

<210> 58

<211> 48

<212> DNA  
 <213> Artificial Sequence

<220>  
 <223> nucleotide sequence coding for a mutant CDR3  
 region

<400> 58  
 gcgaaacata ccgggggggg ccgtcgtatt tgtcatgact actggggc 48

<210> 59  
 <211> 16  
 <212> PRT  
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<220>  
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<221> VARIANT  
 <222> 8, 10, 11  
 <223> Xaa indicates end of amino acid sequence because  
 mutation in nucleotide sequence forms a  
 translational stop codon

<400> 59  
 Ala Lys His Thr Gly Gly Gly Xaa Arg Xaa Xaa Arg Asp Tyr Trp Gly  
 1 5 10 15

<210> 60  
 <211> 48  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> nucleotide sequence coding for a mutant CDR3  
 region

<400> 60  
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<210> 61  
 <211> 16  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> mutant CDR3 region of an antibody heavychain  
 variable region

<400> 61  
 Ala Lys His Thr Gly Gly Gly Gln Lys Leu Gln Leu Asp Tyr Trp Gly  
 1 5 10 15

<210> 62  
 <211> 48  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> nucleotide sequence coding for a mutant CDR3  
region

<400> 62

gcgaaacata ccgggggggg ccagaagctg cagctggact actggggc

48

<210> 63

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> mutant CDR3 region

<221> VARIANT

<222> 2

<223> Xaa indicates end of amino acid sequence because  
mutation in nucleotide sequence forms a  
translational stop codon; or when designated as  
"s" in the disclosure, Xaa is serine

<400> 63

Ala	Xaa	His	Thr	Gly	Gly	Arg	Gly	Trp	Asp	Pro	Ile	Asp	Tyr	Trp	Gly
1				5				10						15	

<210> 64

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> nucleotide sequence coding for a mutant CDR3  
region

<400> 64

gcgtsacata ccggggggggcg cgggttgggac ccattgact actggggc

48

<210> 65

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> mutant CDR3 region of an antibody heavychain  
variable region

<400> 65

Ala	Asn	Gln	Thr	Gly	Gly	Gly	Val	Trp	Asp	Pro	Ile	Asp	Tyr	Trp	Gly
1				5				10						15	

<210> 66

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> nucleotide sequence coding for a mutant CDR3  
region

<400> 66

gcgaaccaga ctggggggggg cgtttgggac cccattgact actggggc

48

<210> 67

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> mutant CDR3 region of an antibody heavychain  
variable region

<400> 67

Ala Arg His Thr Gly Gly Gly Val Trp Asp Pro Ile Tyr Tyr Trp Gly  
1 5 10 15

<210> 68

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> nucleotide sequence coding for a mutant CDR3  
region

<400> 68

gcgagacata ccggtggggg cgtktgggat cccatatact actggggc

48

<210> 69

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> mutant CDR3 region of an antibody heavychain  
variable region

<400> 69

Ala Lys Pro Thr Gly Gly Gly Ala Trp Asp Pro Ile Asp Tyr Trp Gly  
1 5 10 15

<210> 70

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> nucleotide sequence coding for a mutant CDR3  
region

<400> 70

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48

<210> 71  
 <211> 16  
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<220>  
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 variable region

<400> 71  
 Ala Lys His Thr Gly Val Gly Val Trp His Pro Ile Tyr Tyr Trp Gly  
 1 5 10 15

<210> 72  
 <211> 48  
 <212> DNA  
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<220>  
 <223> nucleotide sequence coding for a mutant CDR3  
 region

<400> 72  
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48

<210> 73  
 <211> 14  
 <212> PRT  
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<220>  
 <223> mutant CDR3 region of an antibody heavychain  
 variable region

<400> 73  
 Ala Lys His Thr Gly Val Gly Val Trp Asp Pro Ile Lys Tyr  
 1 5 10

<210> 74  
 <211> 14  
 <212> PRT  
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<220>  
 <223> mutant CDR3 region of an antibody heavychain  
 variable region

<400> 74  
 Ala Lys His Thr Gly Glu Gly Val Trp Asp Pro Ile Lys Tyr  
 1 5 10

<210> 75  
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 <212> PRT  
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<220>

<223> mutant CDR3 region of an antibody heavychain  
variable region

<400> 75

Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Asp Lys  
1 5 10

<210> 76

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> mutant CDR3 region of an antibody heavychain  
variable region

<400> 76

Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Gly Tyr  
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<210> 77

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> mutant CDR3 region of an antibody heavychain  
variable region

<400> 77

Ala Arg His Thr Gly Gly Gly Val Trp Asp Pro Ile Gly Tyr  
1 5 10

<210> 78

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> mutant CDR3 region of an antibody heavychain  
variable region

<400> 78

Ser Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Gly Tyr  
1 5 10

<210> 79

<211> 14

<212> PRT

<213> Artificial Sequence

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<223> mutant CDR3 region of an antibody heavychain  
variable region

<400> 79

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<213> Artificial Sequence
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<220>  
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variable region

<400> 80  
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<210> 81
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<220>  
<223> mutant CDR3 region of an antibody heavychain  
variable region

<400> 81  
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1 5 10

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<210> 82
<211> 14
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<220>
<223> mutant CDR3 region of an antibody heavychain
      variable region
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<400> 82  
Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Leu Asp Asn  
1 5 10

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<210> 83
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      variable region
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<400> 83  
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<210>	84
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<212>	PRT



<213> Artificial Sequence

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<223> mutant CDR3 region of an antibody heavychain  
variable region

<400> 84

Ala Arg His Thr Gly Gly Gly Val Trp Asp Pro Ile Asn Tyr  
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<210> 85

<211> 14

<212> PRT

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<220>

<223> mutant CDR3 region of an antibody heavychain  
variable region

<400> 85

Ala Lys His Thr Gly Ser Gly Val Trp Asp Pro Ile Asn Tyr  
1 5 10

<210> 86

<211> 14

<212> PRT

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<220>

<223> mutant CDR3 region of an antibody heavychain  
variable region

<400> 86

Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Asn Asp  
1 5 10

<210> 87

<211> 14

<212> PRT

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<220>

<223> mutant CDR3 region of an antibody heavychain  
variable region

<400> 87

Ala Lys His Thr Gly Val Gly Val Trp Asp Pro Met Asn Tyr  
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<210> 88

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> mutant CDR3 region of an antibody heavychain  
variable region

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<210> 89  
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<220>  
 <223> mutant CDR3 region of an antibody heavychain  
 variable region

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 variable region

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 variable region

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<210> 92  
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 variable region

<400> 92  
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<210> 93  
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<220>  
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 variable region

<400> 93  
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<210> 94  
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 variable region

<400> 94  
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 variable region

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 1 5 10

<210> 96  
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 variable region

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<210> 97  
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<223> mutant CDR3 region of an antibody heavychain  
variable region

<400> 97

Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Asp Asp  
1 5 10

<210> 98

<211> 14

<212> PRT

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<223> mutant CDR3 region of an antibody heavychain  
variable region

<400> 98

Val Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Val Tyr  
1 5 10

<210> 99

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variable region

<400> 99

Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Val Asp Tyr  
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<210> 100

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variable region

<400> 100

Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Val Pro  
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<210> 101

<211> 14

<212> PRT

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<223> mutant CDR3 region of an antibody heavychain  
variable region

<400> 101

Val Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Ala Tyr  
 1 5 10

<210> 102  
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 variable region

<400> 102  
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 1 5 10

<210> 103  
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<220>  
 <223> mutant CDR3 region of an antibody heavychain  
 variable region

<400> 103  
 Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Met His Tyr  
 1 5 10

<210> 104  
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<220>  
 <223> mutant CDR3 region of an antibody heavychain  
 variable region

<400> 104  
 Ala Lys His Thr Gly Gly Gly Val Trp Asn Pro Ile Asp Tyr  
 1 5 10

<210> 105  
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 <223> mutant CDR3 region of an antibody heavychain  
 variable region

<400> 105  
 Val Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Asp Tyr  
 1 5 10

<210> 106  
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<212> PRT  
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 variable region

<400> 106  
 Ala Lys His Thr Gly Ala Gly Val Trp Asp Pro Ile Asp Tyr  
 1 5 10

<210> 107  
 <211> 14  
 <212> PRT  
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<220>  
 <223> mutant CDR3 region of an antibody heavychain  
 variable region

<400> 107  
 Ala Gln His Thr Gly Gly Gly Val Trp Asp Pro Ile Gly Tyr  
 1 5 10

<210> 108  
 <211> 14  
 <212> PRT  
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 variable region

<400> 108  
 Ala Lys His Thr Gly Arg Gly Val Trp Asp Pro Ile Asp Tyr  
 1 5 10

<210> 109  
 <211> 14  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> mutant CDR3 region of an antibody heavychain  
 variable region

<400> 109  
 Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Tyr Tyr  
 1 5 10

<210> 110  
 <211> 66  
 <212> DNA  
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<220>  
 <223> VH1C Back eukaryotic primer

<400> 110  
 ggactagtcc tggagtgcgc gcactcccag gtccagctgg tgcagtctgg gggaggcttg 60  
 gtacag 66

<210> 111  
 <211> 73  
 <212> DNA  
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<220>  
 <223> VKexpress-MUC-for primer

<400> 111  
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 tggcccagg gcc 73

<210> 112  
 <211> 35  
 <212> DNA  
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<220>  
 <223> MUC1-VL-Back-APA primer

<400> 112  
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<210> 113  
 <211> 296  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
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<400> 113  
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 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
 1 5 10 15

tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttt agc agc tat 96  
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr  
 20 25 30

gcc atg agc tgg gtc cgc cag gct cca ggg aag ggg ctg gag tgg gtc 144  
 Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45

tca gct att agt ggt agt ggt ggt agc aca tac tac gca gac tcc gtg 192  
 Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val  
 50 55 60

aag ggc cgg ttc acc atc tcc aga gac aat tcc aag aac acg ctg tat 240  
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
 65 70 75 80

ctg caa atg aac agc ctg aga gcc gag gac acg gcc gta tat tac tgt 288  
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
                   85                  90                  95

gcg aaa ga 296  
 Ala Lys

<210> 114  
 <211> 98  
 <212> PRT  
 <213> Homo sapiens

<400> 114  
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 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr  
                   20                  25                  30  
 Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
                   35                  40                  45  
 Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val  
   50                  55                  60  
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
  65                  70                  75                  80  
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
                   85                  90                  95  
 Ala Lys

<210> 115  
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<400> 115  
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 Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly  
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gag ccg gcc tcc atc tcc tgc agg tct agt cag agc ctc ctg cat agt 96  
 Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser  
                   20                  25                  30

aat gga tac aac tat ttg gat tgg tac ctg cag aag cca ggg cag tct 144  
 Asn Gly Tyr Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser  
                   35                  40                  45

cca cag ctc ctg atc tat ttg ggt tct aat cgg gcc tcc ggg gtc cct 192  
 Pro Gln Leu Leu Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro  
   50                  55                  60



gac agg ttc agt ggc agt gga tca ggc aca gat ttt aca ctg aaa atc 240  
 Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile  
 65 70 75 80

agc aga gtg gag gct gag gat gtt ggg gtt tat tac tgc atg caa gct 288  
 Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ala  
 85 90 95

cta caa act cct cct 303  
 Leu Gln Thr Pro Pro  
 100

<210> 116  
 <211> 101  
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<400> 116  
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 Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser  
 20 25 30  
 Asn Gly Tyr Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser  
 35 40 45  
 Pro Gln Leu Leu Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro  
 50 55 60  
 Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile  
 65 70 75 80  
 Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ala  
 85 90 95  
 Leu Gln Thr Pro Pro  
 100